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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  1835
1789.5
1693.5
1670.5
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1564.5
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seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A_Geneseq_0401:*

1: /SIDS6/gcgdata/geneseq/geneseqp/AA1980.DAT:*

2: /SIDS6/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS6/gcgdata/geneseq/geneseqp/AA1982.DAT:*

4: /SIDS6/gcgdata/geneseq/geneseqp/AA1983.DAT:*

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19: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

20: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

21: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

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24: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

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26: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

27: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

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29: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*
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  74.0
73.8
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000
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R40384
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Compugen Ltd
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Chimeric antibody
784.12 Heavy chain
MAb 55.1 heavy cha
MAb 55.1 heavy cha
MATI-FAS MAD HFE7A
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Mouse anti-Fas ant
Murine anti-Fas an
Antibody F19 chime
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777	3032	Y29458	R31023	W85689	W85692	R97376	R43673	W90936	W14940	W14939	в36210	W86003	R24442	R28808	W14938	W14941	W48650	W90926	B14776	W83036	W90935	W90929	B14779	W83037	W90934	W90933	W49816	R43339	Y50166	в08026	077	R66758	0
Humanised anti-IL-	Humanised anti-IL-	immun	Antibody D heavy c	D9D10 heavy chain	MoTAbII fusion pro	Murine anti-BGH MA	Mouse anti-bovine		3F4 (Chimeric) hum	3F4 (Chimeric) hum	Human immune syste	sin	œ	pre-5A8 humanised	ne anti-por	3F4 Human IgG4 exp	-	HFE7		humani		HFE7	Q	5	anti-Fa	Ω	sequen	æ.	haped F1		H52H4-160 murine a	Ω	Chimeric mouse/hum

ALIGNMENTS

OK3T; light chain; humanised antibodies; CDR-grafting.

Monoclonal antibody OK3T heavy chain.

03-OCT-1991 (first entry)

R13061;

R13061 standard; Protein; 468 AA

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DE XXX PRAXX PRAXX
WPI; 1991-222915/30
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21-DEC-1989;
                                                                                                                                                                                    (CELL-) CELLTECH LTD
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89GB-0028874.
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RESULT
R40384
XX R40384
AC R4
AC R4
XX R6
D7 08
D7 08
XX R7
E7 KW 11
F7 F7 F7
F7 F7
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 Region
                             Region
                                                            Peptide
                                                                                                       cytotoxic
                                                                                                                   anti-snake small neurotoxin antibody; heavy chain; IgG2;
immunoglobulin; bispecific bivalent antibody; cell-targetting;
                                                                                                                                                                Monoclonal antibody M(alpha)2-3 Heavy-chain
                                                                                                                                                                                             08-FEB-1994
                                                                                                                                                                                                                                                       R40384 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The OK3T heavy chain sequence was deduced from the cDNA sequence isolated from a library prepared from OK3T producing cells. The library was screened with a probe complementary to a region in the mouse IgG2a constant domain region. The OK3T sequence was used in.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2b; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New humanised antibodies comprising CDR grafted antibody - with heavy and light chains, for use in in vivo therapy and diagnosis
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ekknwvernsyscsvvheglhnhhttksfsrtpgk 468
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                                                                                                                                                                                                                                                                                                                                                            KTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAGAYY-FDYWGQGTTLTVSSA 119
                                                                                                                                                                                                                                                                                                                                                                                      PPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNM 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTH 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                redynstlrvvs \verb|alpiqhqdwmsg| kefkckvnnkdlpapiertiskpkgsvrapqvyvlp|
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                             /label= signal_peptide 20..139
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76.3%;
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Pred. No. 3.26
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es 60; Indels
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                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New immunoglobulin hybrid proteins - with immunoglobulin fragments linked to dimeric protein, for diagnostic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-260351/33
N-PSDB; Q48037.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boulain J, Ducancel
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nes 345; Conser
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                LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPA 238
                                                                             AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 178
                                                                                                                              nenfkgkatltvdtssstaymqlssltsedtavyfcaramgatatlldywgqgttltvss
                                                                                                                                           SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAG--AYYFDYWGQGTTLTVSS 118
                                                                                                                                                                                            qiqlqqsgpelvkpgasvkisckasgytftdyyinwvkqkpgqglkwigwiypasgntky 79
lytlsssvtvtsstwpsqsitcnvahpasstkvdkkieprgp--tikpcppc----kcpa
                                                              akttapsvyplapvcgdttgssvtlgclvkgyfpepvtltwnsgslssgvhtfpavlqsd
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COMMISSARIAT ENERGIE ATOMIQUE.
                                                                                                                                                                                                                                                                                                                                              469 AA;
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/label= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
237..252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= joining
253..362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= constant
                                                                                                                                                                                                                                                                           73.8%; Score 1835; DB 1
75.7%; Pred. No. 6.2e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gillet D,
                                                                                                                                                                                                                                                              44;
                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Menez
                                                                                                                                                                                                                                                                             DB 14;
.2e-111;
                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                               469;
                                                                                                                                                                                                                                                              8;
                                                                 199
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PNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT

298

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RESULT
P83200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
      Modified antibodies (Abs) having an altered Fc region with altered binding affinity for an Fc receptor esp. Fc-gamma-R1 may have the following residues replaced: 234, 235, 236 and 237; 235 by Glu, and at least one of the others by Ala. Those with altered binding affinity for Clq may have an altered CH2 domain in which one of the
                                                                                                                                                                                                             01-DEC-1987;
18-MAR-1987;
                                                                                                                    N-PSDB;
                                                                                                                              WPI; 1988-285543/40
                                                                                                                                                 Winter
                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                          effector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P83200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P83200 standard;
following residues of the heavy chain have been changed
                                                              Example; Fig 3; 42pp;
                                                                                                                                                                                                                                                                           W08807089-A
                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                        Mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                 (MEDI-)
                                                                                                                                                                                           10-AUG-1987;
18-MAR-1988;
                                                                                                                                                                                                                                        18-MAR-1988;
                                                                                                                                                                                                                                                          22-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: | : :|:||:| ||| |:: |: ||:|||
vekknwvernsyscsvvheglhnhhttksfsrtpgk 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hredynstlrvvsalpiqhqdwmsgkefkckvnnkdlpapiertiskpkgsvrapqvyvl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pnllggpsvfifppkikdvlmislspivtcvvvdvseddpdvqiswfvnnvevhtaqtqt
                                                                                                                                                GP,
                                                                                  d IgG c
                                                                                                                                                                  MEDICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoded
                                                                                                                                                                                                                                                                                                                                                                                                                          molecule;
                                                                                                                                               Duncan AR,
                                                                                       class antibody - having at
ne constant portion altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                          87GB-0028042.
87GB-0006425.
87GB-0018897.
88WO-GB00211.
                                                                                                                                                                                   88GB-0025480
                                                                                                                                                                                                                                        88WO-GB00211.
                                                                                                                                                                                                                                                                                                                                                                                                                                  class
                                                                                                                                                                                                                                                                                                                        235.
                                                                                                                                                                                                                                                                                                                               120..234
/label= CH3
                                                                                                                                                                                                                                                                                                                                                           /label= CH1
98..119
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                              /note= "This
                                                                                                                                                                                                                                                                                                                                         /label= hinge
120..234
                                                                                                                                                                                                                                                                                                                                                                                                                                                   by mouse 1gG
                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                         constant region; hea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                  COUNCIL
                                                              English.
                                                                                                                                                                                                                                                                                                               CH3
                                                                                                                                               Burton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341
                                                                                                                                                                                                                                                                                                                                                                                                                        region; heavy chain; complen
                                                                                                                                                                                                                                                                                             residue is
                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ŗ
                                                                                                                                               DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene.
                                                                                                                                                                                                                                                                                             Leu
                                                                                         least one aminoacid to alter an effector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454
                                                                                                                                                                                                                                                                                             in mutant EL235"
                                                                                                                                                                                                                                                                                                                                                                                                                         complement.
to a
                                                                                                                                                                                                                                                                                                                                                                                                                                  Fc receptor;
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RESULT
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ID P9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     residue with a different side chain; 318 (changed to Val) 320 and 322 (changed to Gln). Those with altered lytic properties, as compared with unmodified Ab may have an altered CH2 domain where residue 297 of the heavy chain has been changed to Ala.
The sequence encodes the heavy chain of MAb KS1/4, construct mouse/human chimeric antibodies. KS1/4
                                               Recombinant DNA cpds. chimeric derived from
                                                                                                                                                                                                         EP338767-A.
                                                                                                                                                                                                                                                 Mus.
                                                                                                                                                                                                                                                                   Chimeric antibody
                                                                                                                                                                                                                                                                                                          P93037;
                                                                                                                                                                                                                                                                                                                             P93037 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                            Claim
                                                                             N-PSDB;
                                                                                                          Beavers
                                                                                                                           (ELIL )
                                                                                                                                                21-APR-1988;
                                                                                                                                                                                       25-APR-1989
                                                                                                                                                                                                                             KS1/4; chimeric
                                                                                                                                                                                                                                                                                      14-MAR-1990
                                                                                                                                                                   18-APR-1989;
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                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG
                                                                                      1989-311203/43
                                                                                                                                                                                                                                                                                                                                                                           ysklnmktskwektdsfscnvrheglknyylkktisrspgk
                                                                                                                                                                                                                                                                                                                                                                                               YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDV-----QISWFVNNVEVHT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pnleggpsvfifppnikdvlmisltpkvtcvvvdvseddpdvedppgqiswfvnnvevht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lytmsssvtvpsstwpsqtvtcsvahpassttvdkklepsgpistinpcppckechkcpa 120
                           6;
                                                                                                         ĽS,
                                                                                                                           ELI LILLY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                             N91659
                           page 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                        Bumol TF,
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                               88US-0184522
                                                                                                                                                                   89EP-0303814
                                                                                                                                                                                                                            antibody; heavy chain variable region;
                                                                                                                                                                                                                                                                                                                           protein; 447
                          89pp;
                                                                                                                                                                                                                                                                   heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.0%;
98.5%;
                                               producing
monoclonal
                                                                                                                              ၀
                            English
                                                                                                          Gadski
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Pred. No. 3.8e-108;
0; Mismatches 0;
                                                                                                                                                                                                                                                                   variable
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                                                                                                          RA,
                                               antibodies -
l antibody KSJ
                                                                                                        Weigel
                                                KS1/4
                                                                                                          ВJ
                                                         monoclonal
                                                                                                                                                                                                                                                                                                                                                                             341
is a murine
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antibody

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RESULT
R47450
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Best Local
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                                               (CITY )
(YANG/)
WPI; 1994-007204/01
                  Yang
                    Fischer R,
Yang YH;
                                                                                                                  23-DEC-1993.
                                                                                                                                     WO9325237-A.
                                                                                                                                                                          region;
                                                                                                                                                                                   Chimeric;
                                                                                                                                                                                                        T84.12
                                                                                                                                                                                                                         24-JUN-1994
                                                                                                                                                                                                                                             R47450
                                                                                                                                                                                                                                                               R47450 standard; Protein; 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which binds to surface antigens on adenocarcinoma cells and the use human C regions avoids immunological problems during treatment.
                                                                            15-JUN-1992;
                                                                                               15-JUN-1993;
                                                                                                                                                                                                                                                                                                               413
                                                                                                                                                                                                                                                                                                                                  420
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                                                                                                                                                                                                                                                                                                              ekknwvernsyscsvvqeglhnhhttksfsrtpgk 447
                                                                                                                                                                                                                                                                                                                         KTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                   REDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317;
                                                                                                                                                                                                                                                                                                                                                                                         redynstlrvvs alpiqhqdwmsgkefkckvnnkdlpapiertiskpkgsvrapqvyvlp
                                                                                                                                                                                                                                                                                                                                                                                                                              nllggpsvf1fppkikdvlmislspivtcvvvdvseddpdvqiswfvnnvevhtaqtqth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ytlsssvtvtsstwpsqsitcnvahpasstkvdkkieprgp--tikpcppc----kcpap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPKFKGKATLTVDKSSSTAYMELRS-LTSEDSAVYYCARRAGAYYFDYWGQGTTLTVSSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qiqlvqsgpelkkpgetvkisckasgytftnygmnwvkqtpgkglkwmgwintytgepty
                                               CITY
YANG
                                                                                                                                                                         c; carcinoembryonic antigen; CCA; murine; mouse; constant;
transform; myeloma cell; light chain; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447 AA;
                             Paxton
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                                               Y.
                                                                                                                                                                                                       chain
                                                                                                                                                                                                                         (first entry)
                                                                            92US-0904074
                                                                                               93WO-US05709
                                                         HOPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.1%;
69.7%;
                             Shively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55;
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Pred. No. 8e-102
                                                                                                                                                                                                                                                               AA
                             JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                            핕
                            A,
                            Yang
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RESULT
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Best Local (
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       Antigen binding structure; complementarity determining region; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monoclonal antibody; MAb; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering;
                                                                                                 21-NOV-1995
                                                                                                                                                  R76088 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour imaging and immunotherapy.

The amino acid sequence given in the specification hincorrectly identified as a nucleac acid sequence, tunacceptable characters have been represented as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences (Q54651-52) show the light and heavy of murine T84.12. The T84.12 antibody is directed tumour marker carcinoma embryonic antigen, and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chimaeric T84.12 antibody active against carcinoembryonic antigen - has murine variable and human constant regions, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The amino acid sequence given below has been derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; Q54652
                                                                                                                                                                                                                            417 LNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                  440
                                                                                                                                                                                                                                                                                                                  320.qthredynstlrvvsalpiqhqdwmsgkefkckvnnkdlpapiertiskpkgsvrapqvy
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                                                                                                                                                                                                                                                                                                                                                                                                                   QTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVY
                                                                                                                                                                                                                                                                                         ILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSK
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                                                                                                                                                                                                                                                                                                                                                                   PAPNLEGGPSVETFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vdsvkgrftvsrdnarnilylqmsslrsedtamyycari--dyyggggfgywgggtlatv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAGAYY ---- FDYWGQGTTLTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
                                                                                                                                                                                                               lrvekknwvernsyscsvvheglhnyhttksfsrtpgk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the indexer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                 (first entry)
                                                                        chain.
                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.2%; Score 1670.5; 69.0%; Pred. No. 2.6; tive 54; Mismatches
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es 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heavy chain cDNAs
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Matches 304
                                                                                                                                                                                                                                                                                                                                                                   antigen CA55.1. cDNAs for the heavy (094037) and light (094036) chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or V-min humanized 55.1 constructs have been expressed in myeloma cells and E. coll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen binding structures containing CDRs recognising the CA55 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig.15; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-215262/28.
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03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                    Sequence
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          LPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKL
                                                                                                                       THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI
                                                                                 vpevs---svfifppkpkdvltitltpkvtcvvvdiskddpevqfswfvddvevhtaqtq
                                                                                           APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 297
                                                                                                                                                                  EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
ippp keqmakdkvs \texttt{ltcmitd} fiped \texttt{itvewqwngqpaenykntqpimdtdgsyfvyskl}
                                        preeqfnstfrsvselpimhqdwlngkefkcrvnsaafpapiektisktkgrpkapqvyt\\
                                                                                                                                                                                        SAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQS 177
                                                                                                                                                                                                                               SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAR-RAGAY--YFDYWGQGTTLTVS 117
                                                                                                                                                                                                                                                   qvqlqqpgaelvkpgasvqlsckasgytftgywihwvkqrpgqglewigevnpstgrsdy 79
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93GB-0024819
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20..464
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/note= "claim 3, page
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                                                                                                                                                                                                                                                                                                          64.18;
66.58;
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                                                                                                                                                                                                                                                                                                55;
                                                                                                                                                                                                                                                                                              Score 1594.5;
Pred. No. 2e-9:
55; Mismatches
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                                                                                                                                                                                                                                                                                                          2e-95;
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Best Local Similarity
                                                                                                                                                                                                                                        An antigen binding structure is based on the CDRs (given in R76078-84) of the heavy (R76085) and light (R76086) chains of MAb 55.1 (BCACC 93081901), which recognises the colorectal tumor-associated antigen CA55.1. It is optionally humanized and in the form F(ab')2, Fab, Fy, scFv or V-min, and is produced in transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA55.1; colorectal cancer; tumor-associated antigen; hybrido; monoclonal antibody; MAb; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering;
                                                                                                                                                                                                                                                                                                           Claim 3; Page 97-98; 121pp; English.
                                                                                                                                                                                                                                                                                                                                Antigen binding structures containing antigen - produced by hybridomas and I diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-215262/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-1994;
03-DEC-1993;
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                    SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAR-RAGAY--YFDYWGQGTTLTVS 117
                                                                                                        qvqlqqpgaelvkpgasvqlsckasgytftgywihwvkqrpgqglewigevnpstgrsdy 60
                                                                                                                               EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
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                                                               nekfknkatltvdkssttaymqlssltsedsavyycareraygyddamdywgqgtsvtvs
                                           SAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQS
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93GB-0024819
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                                                                                                                                                    Score 1590.5; DB 16;
Pred. No. 3.5e-95;
54; Mismatches 84;
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08-OCT-1997;
01-APR-1997;
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                                                                                                                                                                                                                                                                                           Key
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glomerular nephritis; hypoplastic anaemia; hepatitis;
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apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-Fas MAb HFE7A heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                           scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
                                                                                                                                                                                                                                                                                                                                                                                                                      systemic lupus erythematosus; graft versus host disease;
Sjogren syndrome; pernicious anaemia; Addison's disease;
                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis; autoimmune haemolytic anaemia;
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97JP-0276064.
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20..464
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/note= "claim 9"
118..128
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20..140
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                                                                                                        /label- CDR_H3
/note= "claim 9"
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C Rha by RT-CR (see V70125-26). The invention provides humanised HFETA antibodies (see W8301-37) produced by CDR grafting. These C antibodies are capable of inducing apoptosis in abnormal cells cells. They are used to evaluate, in animal models, treatments of C expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of CC diseases that involve Fas/Fas ligand interactions, and also to treat CC such diseases, including autoimmune disease (e.g. systemic lupus c systematosus, Hashimoto's disease, graft versus host disease, CC siggren syndrome, pernicious anaemia, Addison's disease, rheumatoid CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic c anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 298; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                               LPPPABQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKL 417
                                                                                                                           THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI 357
                                                                                                                                                                                                                                                     GLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCP
                                                                                                                                                                                                                                                                                                SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARR----AGAYYFDYWGQGTTLTVS 117
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                                                                                                                                                                                                                                     dlytlsssvtvpsstwpsqtvtcnvahpasstkvdkkivp----rdc-gckpc-ict
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                                               ipppkeqmakdkvsltcmitdffpeditvewqwngqpaenykntqpimntngsyfvyskl
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Pred. No. 1.7e-93;
B; Mismatches 86; II
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!, Tohru
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B14747
                                                                                                                                                                                                                                                                                                        The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component The anti-Fas antibody as the active component The anti-Fas antibody as the active component antibody HFE7A, or a humanised version of HFE7A containing identical CDRs or a humanised version of HFE7A containing identical CDRs or a humanised version of HFE7A containing identical CDRs or a humanised version of HFE7A containing identical CDRs or a humanised version of HFE7A containing identical CDRs or a humanised version of HFE7A containing identical CDRs or a humanisty determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, and organ graft rejection. The present sequence represents the heavy chain of the murine anti-human Fas monoclonal antibody HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828).
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Best Local
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SAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQS
                                                             qvqlqqpgaelvkpgasvklsckasgytftsywmqwvkqrpgqglewigeidpsdsytny
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panmyelophthisis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
                                                                                                                        New humanized anti-Fas antibody, useful for treating inflammatory or autoimmune disease, induces apoptosis
                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                         Serizawa N,
                                                                                                                                                                                                                                                             30-SEP-1998;
30-SEP-1998;
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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas, ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding bet Fas and its ligand. The products of the invention have anti-inflamed to the system of th

inhibiting binding between ention have anti-inflammatory,

Fas/Fas

Example

reference

4; Page 100-102; 263pp; English.

with abnormal Fas-Fas ligand

systems

apoptosis

selectively

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _
                                                                                                                                                                                                                                                                                                               nvqksnweagntftcsvlheglhnhhtekslshspgk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVQLQQSGPELVKPGASVMISCRTSAYIFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
                                                                                                                                                                                                                                                                                                                                                                                                               THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dlytlsssvtvpsstwpsqtvtcnvahpasstkvdkkivp----rdc-gckpc-ict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARR---AGAYYFDYWGQGTTLTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sakttppsvyplapgsaaqtnsmvtlgclvkgyfpepvtvtwnsgslssgvhtfpavlqs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nqkfkgkatltvdtssstaymqlssltsedsavyycarnrdysnnwyfdvwgtgttvtvs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                          chimeric mouse/human heavy chain variable region (chf19HC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antidiabetic, anti-allergic, anti-arthritic, antiviral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1564.5; DB Pred. No. 1.7e-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                    464
                                                                                                                                                                                                                                                                                                                                                                    454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21; Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367
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Best Local Similarity
Matches 297; Conserv
                                                                                                                                                                                                                                                                                                                                                            types of epithelial cancer. Although F19 may be useful in vitro, e.g., for diagnosis, its applications for in vivo use in humans are problematic as it elicits a human anti-mouse response which reduces the efficacy of the antibody in patients and impairs continued administration. This chimeric antibody was humanised by joining entire murine variable regions to human constant regions. However, humanised antibodies produced by this method can still elicit an anti-mouse response in humans, whereas antibodies humanised via CDR (complementarity determining region) grafting are less immunogenic in humans. Humanised F19 antibodies are useful for treating cancers e.g., colorectal cancers, non-small cell lung cancers, breast cancers, head and neck cancers, ovarian cancers. They are also useful for the detection of activated stromal fibroblasts in a healing wound, inflamed skin or a tumour in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the heavy chain variable region of a chimeric mouse/human F19 antibody (chF19HC). F19 (ATCC Accession number HB 8269) is a murine monoclonal antibody against fibroblast activation protein alpha (FAP). FAP is a cell surface molecule of reactive stromal fibroblasts, and its induction is a highly consistent molecular trait of the reactive stroma of many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         humanisation; complementarity determining region; CDR; CDR grafting; reactive stroma; fibroblast; epithelial cancer; diagnosis; immune response; framework sequence; constant region; variable region; producibility; treatment; cancer; colorectal; lung; breast; head; neck; ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing; skin inflammmation; tumour; immunogenicit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Mus :
Chimeric - Homo
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 18; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibody protein, useful for treating presence of activated stromal fibroblasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-621833/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Park JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chimeric; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP; humanisation; complementarity determining region; CDR; CDR grafting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP953639-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
                                     116 VSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALL 175
                                                                           61
                                                                                                                                                       -
                                                                                                                                                                                             N
vssastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgaltsgvhtfpavl
                                                                           qkfkgratltvgkssstayme.
                                                                                                                 PKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAGAYYF-----DYWGQGTTLT 115
                                                                                                                                                   VQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIFS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garin-Chesa P,
                                                                                                                                                                                                                                                                                                                              453 AA;
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98EP-0107925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                         62.7%; Score 1559; DB 20; 64.6%; Pred. No. 3.8e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bamberger U,
                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leger 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer and in healing
                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for imaging wound or inflamed
                                                                                                                                                                                                                                                                           453;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
Y50157
  Park JE,
                                                                                             30-APR-1998;
                                                                                                                                                                                        03-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric mouse/human F19 antibody heavy chain.
                                             (BOEH ) BOEHRINGER INGELHEIM INT GMBH
                                                                                                                                        30-APR-1998;
                                                                                                                                                                                                                                EP953639-A1
                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune response; framework sequence; constant region;
variable region; producibility; treatment; cancer; colorectal;
breast; head; neck; ovarian; lung; bladder; pancreatic; metast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reactive stroma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody; monoclonal; F19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y50157 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   numanisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||| : |:|::: |||:| || | |:|::| ||||
skitvdksrwqqgnvfscsvmhealhnhytqkslslspgk 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt ktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepq}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQ
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  Garin-Chesa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oclonal; F19; fibrinogen activation protein alpha; complementarity determining region; CDR; CDR graftma; fibroblast; epithelial cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp.
no sapiens.
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                                                                                                                                      98EP-0107925
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143..144
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118..1
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69..85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Leader peptide"
20..472
                                                                                                                                                                                                                                                                                                   144..472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                              /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                    ..132
P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mature mouse F19 heavy chain variable region
                                                                                                                                                                                                                                                                                                                       "mRNA splicing
between these
                                                                                                                                                                                                                                                                                                                                                                                              "CDR 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                       "CDR 2"
                                                                                                                                                                                                                                                                            "Human gamma-1 heavy chain constant region'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complementarity determining
Bamberger U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammmation;
                                                                                                                                                                                                                                                                                                                       residues"
Leger 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour;
                                                                                                                                                                                                                                                                                                                                               Ala
Saldanha
                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region (CDR) 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F19 heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunogenicity;
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                                                                                                                                                                                                                                                                                                                                            inserted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is a highly consistent molecular trait of the reactive stroma of many types of epithelial cancer. Although F19 may be useful in vitro, e.g., for diagnosis, its applications for in vivo use in humans are problematic as it elicits a human anti-mouse response which reduces the efficacy of the antibody in patients and impairs continued administration. This chimeric antibody was humanised by joining entire murine variable regions to human constant regions. However, humanised antibodies produced by this method can still elicit an anti-mouse response in humans, whereas antibodies humanised via CDR (complementarity determining region) grafting are less immunogenic in humans. Humanised T19 antibodies are useful for concernal contracts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the heavy chain of a chimeric mouse/immune antibody. F19 (ATCC Accession number HB 8269) is a murine monoclonal antibody against fibroblast activation protein alpha (FAP). FAP is a antibody against fibroblast activation for the sequence of the induction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating cancers e.g., colorectal cancers, non-small cell lung cancers, breast cancers, head and neck cancers, ovarian cancers, lung cancers, bladder cancers, panoreatic cancers and metastatic cancers the cancers plader cancers, bladder cancers, blad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        surface molecule of reactive stromal fibroblasts, and its induction
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432
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                                                                                                                                                                                                                                                                                                                                                          EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF
                                                           YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                       QVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFI 413
                                                                                                                                                                                                                                            aktkpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprep
                                                                                                                                                                                                                                                                        AQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tvsss-tkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgaltsgvhtfpav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPAL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAGAYYF-----DYWGQGTTL 114 : |||||||||::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   evqlqqsgpelvkpgasvkmscktsrytfteytihwvrqshgkslewigginpnngipny 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           healing wound,
                                                                                                                       qvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppvldsdgsffl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkt-htcpp----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nqkfkgratltvgkssstaymelrsltsedsavyfcarrriaygydeghamdywgqgtsv
yskltvdksrwqqgnvfscsvmhealhnhytqkslslspgk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472
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                               <u>...</u> ... ... ... ... ... ... ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflamed skin or a tumour in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for treating stromal fibroblasts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1550.5; DB 20;
Pred. No. 1.4e-92;
Pred. No. 1.4e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer and in healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20; Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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RESULT R66758

R66758 standard; Protein; 465

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Best Local
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                                                                                                                                                                                                                                                                                                             Q79929 and Q79930 encode R66757 and R66758, the light and heavy chains of an animal derived anti-tobacco mosaic virus (TMV)
                                                                                                                                                                                                                                                                                                                                                                      Transformed plant producing animal-derived anti-virus antibody esp. tobacco plants producing anti-tobacco mosaic virus monoclonal antibody
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                      monoclonal antibody. The cDNAs were incorporated into plasmid vector, which was incorporated into A. tumefac
                                                                                                                                                                                                                                                                                                                                              Example 2; Pages 14-15; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-1993;
                                                                                                                                                                                                                                                plasmid vector, which was incorporated into A. tumefaciens. The resultant plant expression vector was used to transform tobacco plants, making them TMV resistant, the plants could also be biofarmed for the prodn. of anti-virus antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-040220/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP06319396-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-tobacco mosaic virus monoclonal Ab heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NISB ) JAPAN TOBACCO INC. (KURS ) KURARAY CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tobacco mosaic virus; TMV; monoclonal antibody;
                        140
 177
                                               117
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                                                                                                                                                                               Local Similarity
                                                                                                                             1 EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKC
                   SSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQ 176
                                                                   SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAG----AYYFDYWGQGTTLTV 116
                                                                                                                 qvqlqqsgaelarpgasvklsckasgytftsywmqwvkqrpgqglewigaiypgngdtry 79
                                                                                                                                                                                                                              465 AA;
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus-resistant plants; biofarming.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93JP-0131208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=
20..128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "variable heavy domain"
129..141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142..465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- leader
                                                                                                                                                                              62.3%; Score 1550; DB 16; 64.4%; Pred. No. 1.5e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "J heavy 4 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "constant heavy domain"
                                                                                                                                                                  58;
                                                                                                                                                                    Mismatches
                                                                                                                                                                    ; 68
                                                                                                                                                                                         Length 465;
                                                                                                                                                                                                                                                                                                a Ti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XX
                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                    Matches 294;
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                 Humanisation of antibodies - by molecular modelling of the variable domains and alteration by gene conversion mutagenesis {\sf deg}(x)
                                                                                                                                                                                                                                               antibody H52H4-160.
                                                                                                                                                                                                                                                             The sequence is that of the heavy chain of murine anti-CD18
                                                                                                                                                                                                                                                                                       Disclosure; Fig 6A; 126pp;
                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-018139/02
                                                                                                                                                                                                                                                                                                                                                                                     Carter PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R30774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R30774 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9222653-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H52H4-160 murine anti-CD18 antibody heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-1992;
115 TVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPAL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417
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                                      61 nqrfmdkatlavdkststaymelrsltsedsgiyycarwrglnygfdvryfdvwgagttv 120
                                                                                                                                                  Local Similarity 63.8 mes 294; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                                                                                          EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
                                                      qvqlqqsgpelvkpgasvkiscktsgytfteytmhwmkqshgkslewiggfnpknggssh 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSK 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \verb|tippp| keqmakdkvsltcmitdff| peditvewqwngqpaenykntqpimntngsyfvysk|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qpreeqfnstfrsvselpimhqdwlngkefkcrvnsaafpapiektisktkgrpkapqvy
                                                                                                                                                                                                                     454 AA;
                                                                                                                                                                                                                                                                                                                                                                                    Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rapid;
                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-0715272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92WO-US05126
                                                                                                                                                            62.2%;
63.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454
                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                    59;
                                                                                                                                                  Score 1548; DB Pred. No. 2e-92; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                            DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454
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                                                                                                                                                    94;
                                                                                                                                                    Indels
                                                                                                                                                                           Length
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                           Genetically engineering immunoglobulin (Ig) G/IgG dimers for the treatment of cancers, allergic disorders and autoimmune conditions
                                                                                                      WPI; 2000-514811/46.
N-PSDB; A63531.
                                                                                                                                                                                   Braslawsky GR,
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which inhibits formation of intramolecular disulphide bridges between

csister heavy chains on the same antibody molecule. The dimer is a

chomodimer or heterodimer that is capable of activating components of the

ccomplement system, and has the ability to activate and kill cells via the

ccomplement cascade. The dimer is also capable of binding to Fcgamma

creceptors on cytotoxic effector cells and on host immune cells, and is

cc capable of initiating programmed cell death. The IgG/IgG dimers may be

used to treat allergic disorders, cancers and autoimmune diseases such

as allergic asthma, allergic bronchopulmonary aspergillosis, allergic

crininitis, atopic dermatitis, Crohn's disease, Graves's disease, food

clalergies, allergic contact dermatitis, CLL cancers and/or B-cell

lymphomas. They may also be used to treat a range of other diseases and

classorders such as rheumatoid arthritis, ulcerative colitis, psoriasis,

pigeon breeder's disease, hepatitis, leprosy, Lyme disease, diabetes

mellitus, candidlasis and aplastic anaemia. They are also useful for

induction hyper-cross-libring of membrane antigene and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mellitus, candidiasis and aplastic anaemia. They are a inducing hyper-cross-linking of membrane antigens and preferential killing of selected cell populations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a dimeric anti-CD20 light chain polypeptide. The dimeric immunoglobulin is used in the method of invention. The specification describes a method for producing an immunoglobulin (Ig) G/IgG dimer. The method comprises genetically
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                                                                                                         ILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSK
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